STIC Search Report
Biotech-Chem Library

STIC Database Tracking Number: 109652

TO: Minh-Tam Davis **Location: cm1/8a01/8e12** **Art Unit: 1642** **Friday, December 05, 2003** **Case Serial Number: 09/674237**	**From: Toby Port** **Location: Biotech-Chem Library** **CM1-6A04** **Phone: 308-3534** **toby.port@uspto.gov**

Search Notes

Dear Examiner Davis,

Here are the results of your search.
Please feel free to contact me if you have any questions.

Toby Port

```
Qy      426 TGTCTTAGCACAAATATGGGCGCTAGCGGACATGAATAACGATGGAAGGATGGATCAAGT 485
Db      514 TGTTTTAGCACAGATATGGGCACTAGCTGACATGAATAATGATGGAAGAATGGATCAAGT 573

Qy      486 GGAATTTTCCATAGCCATGAAGCTTATCAAACTGAAGCTACAAGGATATCAGCTCCCCTC 545
Db      574 GGAGTTTTCCATAGCTATGAAACTTATCAAACTGAAGCTACAAGGATATCAGCTACCCTC 633

Qy      546 CACACTTCCCCCTGTCATGAAACAGCAACCAGTGGCTATTTCCAGTGCACCAGCATTTGG 605
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Qy      606 TATAGGAGGGATTGCTAGCATGCCACCACTCACAGCTGTTGCTCCTGTGCCAATGGGCTC 665
Db      692 ------------------------------------------------------------ 691

Qy      666 CATTCCAGTTGTTGGAATGTCTCCACCCTTAGTATCTTCTGTCCCTCCAGCAGCAGTGCC 725
Db      692 ----------------------------------------------------GCAGCTGTGCC 702

Qy      726 TCCCCTGGCTAACGGGGCTCCTCCCGTCATACAGCCTCTGCCTGCGTTTGCGCATCCTGC 785
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Qy      786 AGCCACATGGCCAAAGAGTTCTTCCTTCAGCAGATCTGGTCCAGGGTCACAATTAAACAC 845
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Qy      846 TAAGTTACAGAAGGCACAATCATTCGATGTCGCCAGCGCCCCTCCAGCAGCAGAATGGGC 905
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Qy      906 TGTGCCTCAGTCATCAAGGCTGAAATACAGGCAGTTATTCAACAGCCACGACAAAACTAT 965
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Qy     1026 GGCTCAGCTGGCTTCAATATGGAATCTTTCTGACATTGATCAAGATGGAAAACTCACTGC 1085
Db     1003 GGCTCAGCTGGCTTCAATATGGAATCTTTCTGACATTGATCAAGATGGAAAACTTACAGC 1062

Qy     1086 AGAAGAATTTATCCTAGCTATGCACCTAATTGATGTTGCCATGTCTGGTCAGCCACTGCC 1145
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Qy     1206 GATGTCCGTCATAAGCTCTTCTTCTGTGGATCAGAGGCTGCCTGAGGAGCCGTCGTCAGA 1265
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Qy     1266 GGATGAGCAGCAGC---CAGAGAAGAAACTGCCTGTGACATTTGAAGATAAGAAGCGGGA 1322
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Qy     1323 GAACTTCGAGCGAGGCAGTGTGGAGCTGGAGAAGCGCCGCCAAGCGCTCTTGGAGCAGCA 1382
Db     1303 GAACTTTGAACGTGGCAACCTGGAACTGGAGAAACGAAGGCAAGCTCTCCTGGAACAGCA 1362

Qy     1383 GCGCAAAGAGCAGGAGCGGTTGGCTCAGCTGGAGCGCGCCGAGCAGGAGAGGAAAGAGCG 1442
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Qy     1623 ACTCCTGAATCAGAGGAACAAGGAGCAGGAGGGCACCGTGGTCCTGAAGGCAAGGAGGAA 1682
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Qy     1923 GCAGAACAGTTTGCATAGAGACTCGCTTCTTACCCTCAAAAGAGCCTTGGAAGCAAAGGA 1982
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Db     1963 ACTAGCTCGGCAGCACCTACGAGACCAACTGGATGAAGTGGAGAAAGAAACTAGATCAAA 2022

Qy     2043 GCTGCAGGAGATTGATGTTTTCAACAACCAGCTGAAGGAACTGAGAGAGATACATAGCAA 2102
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Db     2083 GCAACAACTCCAGAAGCAAAAGTCCATGGAGGCTGAACGACTGAAACAG 2131
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RESULT 14
HSU61166

LOCUS	HSU61166 3241 bp mRNA linear PRI 23-JUL-1996
DEFINITION	Human SH3 domain-containing protein SH3P17 mRNA, complete cds.
ACCESSION	U61166
VERSION	U61166.1 GI:1438932
KEYWORDS	.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1 (bases 1 to 3241)
AUTHORS	Sparks,A.B., Hoffman,N.G., McConnell,S.J., Fowlkes,D.M. and Kay,B.K.
TITLE	Cloning of ligand targets: systematic isolation of SH3 domain-containing proteins
JOURNAL	Nat. Biotechnol. 14 (6), 741-744 (1996)
MEDLINE	98294438
PUBMED	9630982
REFERENCE	2 (bases 1 to 3241)
AUTHORS	Pirozzi,G., McConnell,S.J., Uveges,A. and Fowlkes,D.M.
TITLE	Direct Submission
JOURNAL	Submitted (18-JUN-1996) CYTOGEN Corp., 307 College Road East, Princeton, NJ 08540, USA

FEATURES	Location/Qualifiers
source	1. .3241 /organism="Homo sapiens" /mol_type="mRNA"

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                     /tissue_type="bone marrow"
     CDS             37. .1599
                     /codon_start=1
                     /product="SH3 domain-containing,protein SH3P17"
                     /protein_id="AAC50592.1"
                     /db_xref="GI:1438933"
                     /translation="MEAERLKQKEQERKIIELEKQKEEAQRRAQERDKQWLEHVQQED
                     EHQRPRKLHEEEKLKREESVKKKDGEEKGKQEAQDKLGRLFHQHQEPAKPAVQAPWST
                     AEKGPLTISAQENVKVVYYRALYPFESRSHDEITIQPGDIVMVDESQTGEPGWLGGEL
                     KGKTGWFPANYAEKIPENEVPAPVKPVTDSTSAPAPKLALRETPAPLAVTSSEPSTTP
                     NNWADFSSTWPTSTNEKPETDNWDAWAAQPSLTVPSAGQLRQRSAFTPATATGSSPSP
                     VLGQGEKVEGLQAQALYPWRAKKDNHLNFNKNDVITVLEQQDMWWFGEVQGQKGWFPK
                     SYVKLISGPIRKSTSMDSGSSESPASLKRVASPAAKPVVSGEEIAQVIASYTATGPEQ
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                     VKLTTDMDPSQQ"
BASE COUNT      994 a    756 c    702 g    789 t
ORIGIN

  Query Match             24.6%;  Score 1252.6;  DB 9;  Length 3241;
  Best Local Similarity   69.8%;  Pred. No. 9.2e-277;
  Matches 2132;  Conservative    0;  Mismatches  604;  Indels  317;  Gaps   20;

Qy       2112 CCAGAAGCAGAGGTCCCTGGAGGCAGCGCGACTGAAGCAGAAAGAGCAGGAGAGGAAGAG 2171
Db         21 CCAGAAGCAAAAGTCCATGGAGGCTGAACGACTGAAACAGAAAGAACAAGAACGAAAGAT 80

Qy       2172 CCTGGAGTTAGAGAAGCAAAAGGAAGACGCTCAGAGACGAGTTCAGGAAAGGGACAAGCA 2231
Db         81 CATAGAATTAGAAAAACAAAAAGAAGAAGCCCAAAGACGAGCTCAGGAAAGGGACAAGCA 140

Qy       2232 ATGGCTGGAGCATGTGCAGCAGGAG---GAGCAGCCACGCCCCCGGAAACCCCACGAGGA 2288
Db        141 GTGGCTGGAGCATGTGCAGCAGGAGGACGAGCATCAGAGACCAAGAAAACTCCACGAAGA 200

Qy       2289 GGACAGACTGAAGAGGGAAGACAGTGTCAGGAAGAAGGAGGCGGAAGAGAGAGCCAAGCC 2348
Db        201 GGAAAAACTGAAAAGGGAGGAGAGTGTCAAAAAGAAGGATGGCGAGGAAAAAGGCAAACA 260

Qy       2349 GGAAATGCAAGACAAGCAGAGTCGGCTTTTCCATCCGCATCAGGAGCCAGCTAAGCTGGC 2408
Db        261 GGAAGCACAAGACAAGCTGGGTCGGCTTTTCCATCAACACCAAGAACCAGCTAAGCCAGC 320

Qy       2409 CACCCAGGCACCCTGGTCTACCACAGAGAAAGGCCCGCTTACCATTTCTGCACAGGAGAG 2468
Db        321 TGTCCAGGCACCCTGGTCCACTGCAGAAAAAGGTCCACTTACCATTTCTGCACAGGAAAA 380

Qy       2469 TGTAAAAGTGGTATATTACCGAGCGCTGTACCCCTTTGAATCCAGAAGTCACGATGAGAT 2528
Db        381 TGTAAAAGTGGTGTATTACCGGGCACTGTACCCCTTTGAATCCAGAAGCCATGATGAAAT 440

Qy       2529 CACCATCCAGCCAGGAGATATAGTCATGGTGGATGAAAGCCAGACTGGAGAGCCAGGATG 2588
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Qy       2589 GCTTGGAGGAGAGCTGAAAGGGAAGACGGGATGGTTCCCTGCAAACTATGCAGAAAAGAT 2648
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Qy       2649 TCCAGAAAATGAGGTTCCCACTCCAGCCAAACCAGTGACCGATCTGACATCTGCCCCTGC 2708
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Qy       2769 CACAACCCCCAACAACTGGGCAGACTTCAGTTCCACGTGGCCCAGCAGCTCAAACGAGAA 2828
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Qy       2829 GCCAGAAACGGACAACTGGGATACGTGGGCGGCTCAGCCTTCTCTGACCGTACCTAGTGC 2888
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Qy       2889 TGGCCAGTTACGGCAGAGATCAGCCTTTACCCCAGCCACAGCCACTGGCTCCTCCCCATC 2948
Db        801 CGGCCAGTTAAGGCAGAGGTCCGCCTTTACTCCAGCCACGGCCACTGGCTCCTCCCCGTC 860

Qy       2949 TCCCGTCCTGGGCCAGGGTGAAAAGGTGGAAGGGCTACAAGCGCAAGCCCTGTATCCCTG 3008
Db        861 TCCTGTGCTAGGCCAGGGTGAAAAGGTGGAGGGGCTACAAGCTCAAGCCCTATATCCTTG 920

Qy       3009 GAGAGCCAAAAAAGACAACCACTTAAATTTTAACAAAAGTGACGTCATCACCGTTCTGGA 3068
Db        921 GAGAGCCAAAAAAGACAACCACTTAAATTTTAACAAAAATGATGTCATCACCGTCCTGGA 980

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Db        981 ACAGCAAGACATGTGGTGGTTTGGAGAAGTTCAAGGTCAGAAGGGTTGGTTCCCCAAGTC 1040

Qy       3129 TTACGTGAAACTCATTTCAGGGCCCGTAAGGAAATCCACAAGCATCGATACTGGCCCTAC 3188
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Qy       3189 TGAAAGTCCTGCTAGTCTAAAGAGAGTGGCTTCCCCGGCCGCCAAGCCAGCCATTCCCGG 3248
Db       1101 AGAGAGTCCTGCTAGTCTAAAGCGAGTAGCCTCTCCAGCAGCCAAGCCGGTCGTTTCGGG 1160

Qy       3249 AGAAGAGTTTATTGCCATGTACACATACCAGAGTTCTGAGCAAGGAGATTTAACCTTTCA 3308
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Qy       3309 GCAAGGGGATGTGATTGTGGTTACCAAGAAAGATGGTGACTGGTGGACGGGAACGGTGGG 3368
Db       1165 ------------------------------------------------------------ 1164

Qy       3369 CGACAAGTCCGGAGTCTTCCCTTCTAACTATGTGAGGCTTAAAGATTCAGAGGGCTCTGG 3428
Db       1165 ------------------------------------------------------------ 1164

Qy       3429 AACTGCTGGGAAAACAGGGAGTTTAGGAAAAAAACCTGAAATTGCCCAGGTTATTGCTTC 3488
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Qy       3489 CTACGCTGCTACTGGTCCCGAACAACTCACCCTGGCTCCTGGGCAGCTGATTCTGATCCG 3548
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Qy       3609 GATAGGGTGGTTTCCAGCAAATTATGTCAAACTTCTAAGCCCCGGAACAAGCAAAATCAC 3668
Db       1308 GATAGGCTGGTTCCCAGCTAATTATGTAAAGCTTCTAAGCCCTGGGACGAGCAAAATCAC 1367

Qy       3669 CCCAACTGAGCTACCCAAGACCGCAGTGCAGCCAGCAGTGTGCCAGGTGATCGGGATGTA 3728
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Qy       3729 CGATTACACCGCCCAGAACGATGACGAACTAGCCTTCAGCAAAGGCCAGATCATCAACGT 3788
Db       1428 CGACTACACCGCGCAGAATGACGATGAGCTGGCCTTCAACAAGGGCCAGATCATCAACGT 1487

Qy       3789 CCTCAACAAGGAGGACCCGGACTGGTGGAAAGGAGAAGTCAGTGGGCAAGTTGGGCTCTT 3848
Db       1488 CCTCAACAAGGAGGACCCTGACTGGTGGAAAGGAGAAGTCAATGGACAAGTGGGGCTCTT 1547

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Qy       3909 TTGTCCATCCCCCCCTCAGGCTTGAAAGTCCTCAAAGAGACCCACTATCCCATATCACTG 3968
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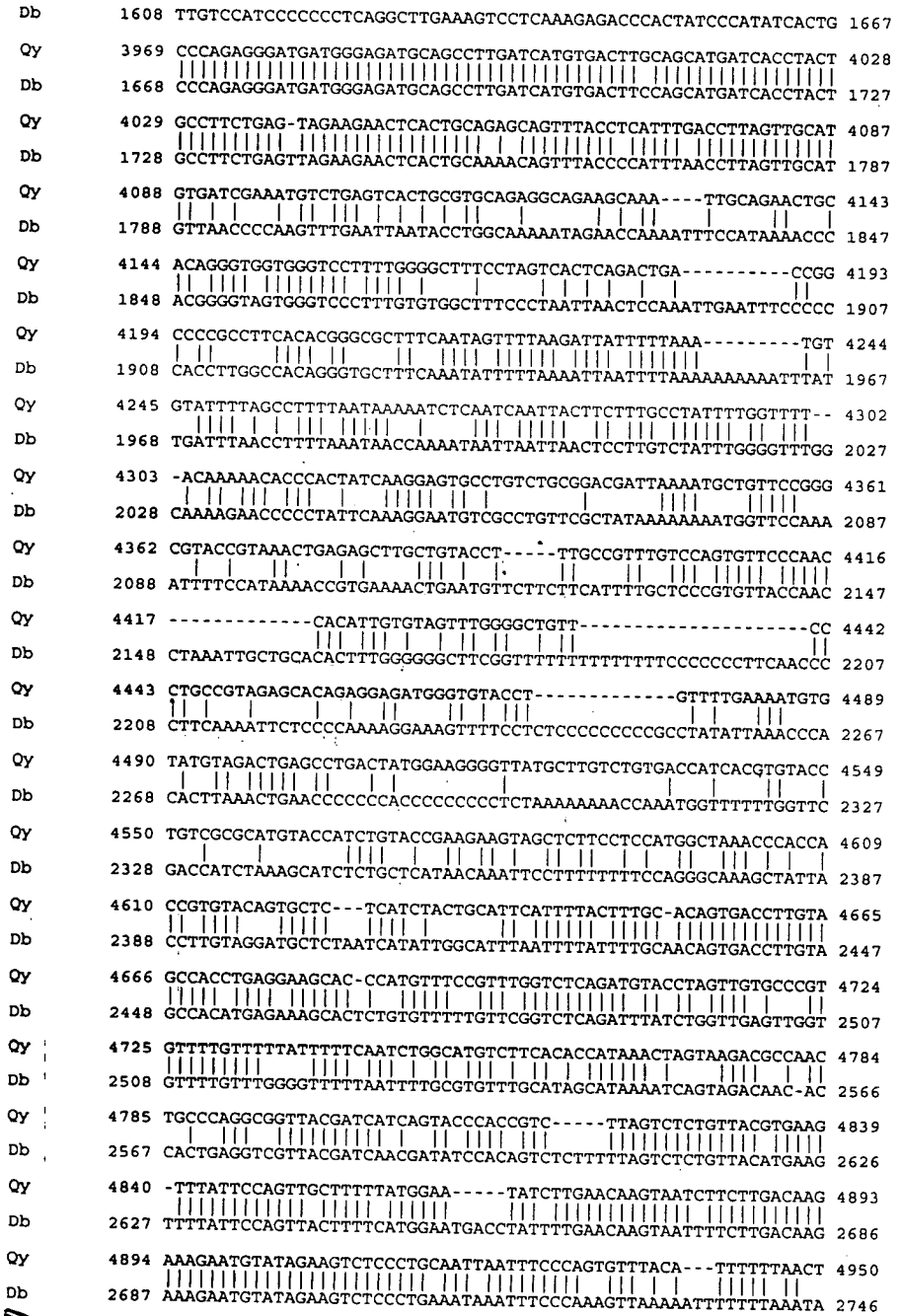

RESULT 15
BD127640
LOCUS BD127640 1676 bp DNA linear PAT 18-SEP-2002
DEFINITION Primer for synthesizing full-length cDNA and use thereof.
ACCESSION BD127640
VERSION BD127640.1 GI:23222585
KEYWORDS JP 2002017375-A/3071.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1676)
AUTHORS Ota,T., Nishikawa,T., Isogai,T., Hayashi,K., Ishii,S., Kawai,Y., Wakamatsu,A., Sugiyama,T., Nagai,K., Kojima,S., Otsuki,T. and Koga,H.
TITLE Primer for synthesizing full-length cDNA and use thereof
JOURNAL Patent: JP 2002017375-A 3071 22-JAN-2002;
HELIX RESEARCH INSTITUTE
COMMENT OS Homo sapiens (human)
PN JP 2002017375-A/3071
PD 22-JAN-2002
PF 07-JUL-2000 JP 2000253172
PI TOSHIO OTA,TETSUO NISHIKAWA,TAKAO ISOGAI,KOJI HAYASHI,SHIZUKO
PI ISHII,
PI YURI KAWAI,AI WAKAMATSU,TOMOYASU SUGIYAMA,KEIICHI NAGAI, PI SHINICHI KOJIMA,
PI TETSUJI OTSUKI,HISASHI KOGA
PC
C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/ PC 10,
PC C12P21/02,C12Q1/68//C12P21/08,G06F17/30,C12N15/00,C12N5/00 CC Primer for synthesizing full-length cDNA and use thereof FH Key Location/Qualifiers
FT CDS (264). .(1676).
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source 1. .1676
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
BASE COUNT 485 a 381 c 458 g 352 t
ORIGIN

Query Match 24.6%; Score 1249.2; DB 6; Length 1676;
Best Local Similarity 85.7%; Pred. No. 5.2e-276;
Matches 1428; Conservative 0; Mismatches 223; Indels 15; Gaps 3;

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Qy       1612 GGAAGACTTATTCCAGAGAAACAGATACTCAGTGACCAGTTAAAACAAGTCCAGCAGAAC 1671

Db       1695 ATCTATCTGGTCCCTGAGAAGCAGCTATTAAACGAAAGAATTAAAAACATGCAGCTCAGT 1754

Qy       1672 AGTTTGCATAGAGACTCGCTTCTTACCCTCAAAAGAGCCTTGGAAGCAAAGGAGCTGGCC 1731

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Qy       1732 CGGCAGCAGCTCCGGGAGCAGCTGGACGAGGTGGAGAGAGAGACCAGGTCAAAGCTGCAG 1791

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Qy       1792 GAGATTGATGTTTTCAACAACCAGCTGAAGGAACTGAGAGAGATACATAGCAAACAGCAA 1851

Db       1875 GAAATGGATTCATTTAACAATCAGCTGAAGGAACTCAGAGAAAGCTATAATACACAGCAG 1934

Qy       1852 CTCCAGAAGCAGAGGTCCCTGGAGGCAGCGCGACTGAAGCAGAAAGAGCAGGAGAGGAAG 1911

Db       1935 TTAGCCCTTGAACAACTTCATAAAATCAAACGTGACAAATTGAAGGAAATCGAAAGAAAA 1994

Qy       1912 AGCCTGGAGTTAGAGAAGCAAAA 1934

Db       1995 AGATTAGAGCAAAAAAAAAAAA 2017
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RESULT 5
US-09-764-881-55
; Sequence 55, Application US/09764881
; Publication No. US20030125246A9
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PTZ07
; CURRENT APPLICATION NUMBER: US/09/764,881
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 192
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 55
; LENGTH: 568
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (481)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (536)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (556)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (562)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-764-881-55

Query Match 9.8%; Score 356; DB 11; Length 568;
Best Local Similarity 86.2%; Pred. No. 5.2e-92;
Matches 426; Conservative 0; Mismatches 64; Indels 4; Gaps 3;

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Qy         61 GAAAGGGCCAAGCATGACCAGCAGTTCCTTAGCCTGAAGCCGATAGCGGGATTTATTACT 120

Db        138 GAAAGAGCGA--CATGATCAGCAGTTCCATAGTTTAAAGCCAATATCTGGATTCATTACT 195

Qy        121 GGTGATCAAGCGAGGAACTTTTTTTTCCAATCTGGGTTACCTCAGCCTGTCTTAGCACAA 180

Db        196 GGTGATCAAGCTAGAAACTTTTTTTTTCAATCTGGGTTACCTCAACCTGTTTTAGCACAG 255

Qy        181 ATATGGGCGCTAGCGGACATGAATAACGATGGAAGGATGGATCAAGTGGAATTTTCCATA 240

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Qy        480 CGGGGCTCCTCCCG 493

Db        555 ANGGGGTNCCCCTG 568
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RESULT 6
US-09-879-957-193
; Sequence 193, Application US/09879957
; Patent No. US20020034755A1
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; HOFFMAN, No. US20020034755A1h
; KAY, Brian K.
; FOWLKES, Dana M.
; McCONNELL, Stephen J.
; TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL
; DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND
; USING SAME
; NUMBER OF SEQUENCES: 227
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/879,957
; FILING DATE: 13-Jun-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/630,915
; FILING DATE: 03-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-174
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864/9741
; TELEX: 66141 PENNIE

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;   INFORMATION FOR SEQ ID NO: 193:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 2873 bases
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: unknown
;        MOLECULE TYPE: DNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 193:
US-09-879-957-193

  Query Match             9.1%;  Score 332.4;  DB 9;  Length 2873;
  Best Local Similarity   61.0%;  Pred. No. 9e-85;
  Matches  631;  Conservative    0;  Mismatches  361;  Indels   42;  Gaps    4;

Qy       2609 CTTCTCTGACCGTACCTAGTGCTGGCCAGTTACGGCAGAGATCAGCCTTTACCCCAGCCA 2668
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Qy       2669 CAGCCACTGGCTCCTCCCCATCTCCCGTCCTGGGCCAGGGTGAAAAGGTGGAAGGGCTAC 2728
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Qy       2789 GTGACGTCATCACCGTTCTGGAACAGCAAGACATGTGGTGGTTTGGAGAAGTTCAAGGTC 2848
Db        718 ATGACATTATTACTGTCTTGGAGCAGCAAGAAAATTGGTGGTTTGGGGAGGTGCATGGAG 777

Qy       2849 AGAAGGGTTGGTTCCCCAAGTCTTACGTGAAACTCATTTCAGGGCCCGTAAGGAAATCCA 2908
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Qy       3269 CTGGGCAGCTGATTCTGATCCGGAAAAAGAACCCAGGTGGATGGTGGGAAGGAGAACTGC 3328
Db       1180 CAGGACAGTTAATATTAATTCTAAAGAAAAATACAAGTGGGTGGTGGCAAGGAGAGTTAC 1239

Qy       3329 AAGCTCGAGGGAAAAAGCGCCAGATAGGGTGGTTTCCAGCAAATTATGTCAAACTTCTAA 3388
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Qy       3389 GCCCCGGAACAAGCAAAATCACCCCAACTGAGCTACCCAAGACCGCAGTGCAGCCAGCAG 3448
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Qy       3449 TGTGCCAGGTGATCGGGATGTACGATTACACCGCCCAGAACGATGACGAACTAGCCTTCA 3508
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Qy       3509 GCAAAGGCCAGATCATCAACGTCCTCAACAAGGAGGACCCGGACTGGTGGAAAGGAGAAG 3568
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Qy       3569 TCAGTGGGCAAGTTGGGCTCTTCCCATCCAATTATGTAAAGCTGACCACAGACATGGACC 3628
Db       1459 TCAACGGGGTGACTGGTCTCTTTCCTTCAAACTACGTTAAGATGACGACAGACTCAGATC 1518

Qy       3629 CCAGCCAGCAATGA 3642
Db       1519 CAAGTCAACAGTGA 1532


RESULT 7
US-09-764-868-125
; Sequence 125, Application US/09764868
; Patent No. US20020168711A1
; GENERAL INFORMATION:
;  APPLICANT: Rosen et al.
;  TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
;  FILE REFERENCE: PTZ32
;  CURRENT APPLICATION NUMBER: US/09/764,868
;  CURRENT FILING DATE:  2001-01-17
;  Prior application data removed - refer to PALM or file wrapper
;  NUMBER OF SEQ ID NOS: 1510
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 125
;   LENGTH: 4210
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-764-868-125

  Query Match             9.1%;  Score 331.4;  DB 10;  Length 4210;
  Best Local Similarity   61.0%;  Pred. No. 2.2e-84;
  Matches  630;  Conservative    0;  Mismatches  361;  Indels   42;  Gaps    4;

Qy       2609 CTTCTCTGACCGTACCTAGTGCTGGCCAGTTACGGCAGAGATCAGCCTTTACCCCAGCCA 2668
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Qy       2669 CAGCCACTGGCTCCTCCCCATCTCCCGTCCTGGGCCAGGGTGAAAAGGTGGAAGGGCTAC 2728
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Qy       2729 AAGCGCAAGCCCTGTATCCCTGGAGAGCCAAAAAAGACAACCACTTAAATTTTAACAAAA 2788
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Qy       2789 GTGACGTCATCACCGTTCTGGAACAGCAAGACATGTGGTGGTTTGGAGAAGTTCAAGGTC 2848
Db       1095 ATGACATTATTACTGTCTTGGAGCAGCAAGAAAATTGGTGGTTTGGGGAGGTGCATGGAG 1154

Qy       2849 AGAAGGGTTGGTTCCCCAAGTCTTACGTGAAACTCATTTCAGGGCCCGTAAGGAAATCCA 2908
Db       1155 GAAGAGGATGGTTTCCCAAATCTTATGTCAAGATCATTCCTGGGAGTGAAGTAAAACGGG 1214

Qy       2909 CAAGCATCGATACTGGCCCTACTGAAAGTCCTGCTAGTCTAAAGAGAGTGGCTTCCCCGG 2968
Db       1215 AA------------GAACCAGAAGCTTTGTATGCAGCTGTAAATAAGAAACCTACCTCGG 1262

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Db       1263 CAGCCTATTCAGTT------GGAGAAGAATATATTGCACTTTATCCATATTCAAGTGTGG 1316

Qy       3029 AGCAAGGAGATTTAACCTTTCAGCAAGGGGATGTGATTGTGGTTACCAAGAAAGATGGTG 3088
Db       1317 AACCTGGAGATTTGACTTTCACAGAAGGTGAAGAAATATTGGTGACCCAGAAAGATGGAG 1376

Qy       3089 ACTGGTGGACGGGAACGGTGGGCGACAAGTCCGGAGTCTTCCCTTCTAACTATGTGAGGC 3148
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SYSTEM:OS  - DIALOG OneSearch
  File 155:MEDLINE(R)  1966-2004/Jan W1
         (c) format only 2003 The Dialog Corp.
*File 155: Medline is updating again (12-22-2003).
Please see HELP NEWS 154, for details.
  File  55:Biosis Previews(R)  1993-2003/Dec W4
         (c) 2003 BIOSIS
  File  34:SciSearch(R) Cited Ref Sci  1990-2003/Dec W4
         (c) 2003 Inst for Sci Info
*File  34: New prices as of 1/1/2004 per Information Provider
request.  See HELP RATES 34.
  File 434:SciSearch(R) Cited Ref Sci  1974-1989/Dec
         (c) 1998 Inst for Sci Info
*File 434: New prices as of 1/1/2004 per Information Provider
request.  See HELP RATES434.
  File 340:CLAIMS(R)/US Patent  1950-03/Dec 30
         (c) 2004 IFI/CLAIMS(R)
*File 340: Enter HELP NEWS340 & HELP ALERTS340 for search,
 display & Alert information.

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Processing
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           39893  SH
         9512958  3
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? s s1 and s2
           50156  S1
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      S3      76  S1 AND S2
? s endocytosis
      S4   44776  ENDOCYTOSIS
? s s3 and s4
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           44776  S4
      S5      46  S3 AND S4
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Processing
Processing
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          988300  MOUSE
        12569368  HUMAN
         2116815  RAT
      S615061011  MAMMALIAN OR MOUSE OR HUMAN OR RAT
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>>>Duplicate detection is not supported for File 340.

>>>Records from unsupported files will be retained in the RD set.
...completed examining records
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S9 3 RD (unique items)
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9/3,K,AB/1 (Item 1 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

11597797 99030416 PMID: 9813051
Intersectin, a novel adaptor protein with two Eps15 homology and five Src homology 3 domains.
Yamabhai M; Hoffman N G; Hardison N L; McPherson P S; Castagnoli L; Cesareni G; Kay B K
Department of Pharmacology, University of Wisconsin, Madison, Wisconsin 53706-1532, USA.
Journal of biological chemistry (UNITED STATES) Nov 20 **1998**, 273 (47) p31401-7, ISSN 0021-9258 Journal Code: 2985121R
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
We screened a Xenopus laevis oocyte cDNA expression library with a Src homology 3 (**SH3**) class II peptide ligand and identified a 1270-amino acid-long protein containing two Eps15 homology (**EH**) domains, a central coiled-coil region, and five **SH3** domains. We named this protein Intersectin, because it potentially brings together **EH** and **SH3** domain-binding proteins into a macromolecular complex. The ligand preference of the **EH** domains were deduced to be asparajine-proline-phenylalanine (NPF) or cyclized NPF (CX1-2NPFXXC), depending on the type of phage-displayed combinatorial peptide library used. Screens of a **mouse** embryo cDNA library with the **EH** domains of Intersectin yielded clones for the Rev-associated binding/Rev-interacting protein (RAB/Rip) and two novel proteins, which we named Intersectin-binding proteins (Ibps) 1 and 2. All three proteins contain internal and C-terminal NPF peptide sequences, and Ibp1 and Ibp2 also contain putative clathrin-binding sites. Deletion of the C-terminal sequence, NPFL-COOH, from RAB/Rip eliminated **EH** domain binding, whereas fusion of the same peptide sequence to glutathione S-transferase generated strong binding to the **EH** domains of Intersectin. Several experiments support the conclusion that the free carboxylate group contributes to binding of the NPFL motif at the C terminus of RAB/Rip to the **EH** domains of Intersectin. Finally, affinity selection experiments with the **SH3** domains of Intersectin identified two endocytic proteins, dynamin and synaptojanin, as potential interacting proteins. We propose that Intersectin is a component of the endocytic machinery.

Nov 20 **1998**,
We screened a Xenopus laevis oocyte cDNA expression library with a Src homology 3 (**SH3**) class II peptide ligand and identified a 1270-amino acid-long protein containing two Eps15 homology (**EH**) domains, a central coiled-coil region, and five **SH3** domains. We named this protein Intersectin, because it potentially brings together **EH** and **SH3** domain-binding proteins into a macromolecular complex. The ligand preference of the **EH** domains were deduced to be asparajine-proline-phenylalanine (NPF) or cyclized NPF (CX1-2NPFXXC), depending on the type of phage-displayed combinatorial peptide library used. Screens of a **mouse** embryo cDNA library with the **EH** domains of Intersectin yielded clones for the Rev-associated binding/Rev-interacting protein (RAB/Rip...

... clathrin-binding sites. Deletion of the C-terminal sequence, NPFL-COOH, from RAB/Rip eliminated **EH** domain binding, whereas fusion of the same peptide sequence to glutathione S-transferase generated strong binding to the **EH** domains of Intersectin. Several experiments support the

conclusion that the free carboxylate group contributes to binding of the NPFL motif at the C terminus of RAB/Rip to the **EH** domains of Intersectin. Finally, affinity selection experiments with the **SH3** domains of Intersectin identified two endocytic proteins, dynamin and synaptojanin, as potential interacting proteins. We...
...Tags: **Human**;
...; Acid Sequence; Binding, Competitive; DNA-Binding Proteins--genetics --GE; DNA-Binding Proteins--metabolism--ME; Dynamins; **Endocytosis**; GTP Phosphohydrolases--metabolism--ME; Gene Library; Ligands; Mice; Molecular Sequence Data; Nerve Tissue Proteins--metabolism...

9/3,K,AB/2 (Item 1 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci

06349691 Genuine Article#: YL419 Number of References: 41
Title: An eps homology (**EH**) domain protein that binds to the Ral-GTPase target, RalBP1 (ABSTRACT AVAILABLE)
Author(s): Yamaguchi A; Urano T; Goi T; Feig LA (REPRINT)
Corporate Source: TUFTS UNIV,SCH MED, DEPT BIOCHEM/BOSTON//MA/02111 (REPRINT); TUFTS UNIV,SCH MED, DEPT BIOCHEM/BOSTON//MA/02111
Journal: JOURNAL OF BIOLOGICAL CHEMISTRY, **1997**, V272, N50 (DEC 12), P 31230-31234
ISSN: 0021-9258 Publication date: 19971212
Publisher: AMER SOC BIOCHEMISTRY MOLECULAR BIOLOGY INC, 9650 ROCKVILLE PIKE, BETHESDA, MD 20814
Language: English Document Type: ARTICLE
Abstract: Ral proteins constitute a family of small GTPases that can be activated by Ras in cells, In the GTP-bound state, Ral proteins bind to RalBP1, a GTPase-activating protein for CDC42 and Rac GTPases. We have used the two-hybrid system in yeast to clone a cDNA for a novel similar to 85-kDa protein that can bind to an additional site on RalBP1, This newly identified protein contains an Eps homology (**EH**) domain, which was first detected in the epidermal growth factor (EGF) receptor substrate Eps15. Recently, the **EH** domain of Eps15 has been shown to bind to proteins containing an asparagine-proline-phenylalanine motif. Moreover, **EH** domains have been found in proteins involved in **endocytosis** and/or actin cytoskeleton regulation. The RalBP1 associated Eps-homology domain protein, Reps1, is tyrosine-phosphorylated in response to EGF stimulation of cells. In addition, Reps1 has the capacity to form a complex with the **SH3** domains of the adapter proteins Crk and Grb2, which may link Reps1 to an EGF-responsive tyrosine kinase. Thus, Reps1 may coordinate the cellular actions of activated EGF receptors and Ral-GTPases.

Title: An eps homology (**EH**) domain protein that binds to the Ral-GTPase target, RalBP1
, **1997**
...Abstract: bind to an additional site on RalBP1, This newly identified protein contains an Eps homology (**EH**) domain, which was first detected in the epidermal growth factor (EGF) receptor substrate Eps15. Recently, the **EH** domain of Eps15 has been shown to bind to proteins containing an asparagine-proline-phenylalanine motif. Moreover, **EH** domains have been found in proteins involved in **endocytosis** and/or actin cytoskeleton regulation. The RalBP1 associated Eps-homology domain protein, Reps1, is tyrosine...

...stimulation of cells. In addition, Reps1 has the capacity to form a complex with the **SH3** domains of the adapter proteins Crk and Grb2, which may link Reps1 to an EGF...
...Identifiers--NUCLEOTIDE DISSOCIATION STIMULATOR; TYROSINE KINASE SUBSTRATE; ACTIVATING PROTEIN; PUTATIVE EFFECTOR; **SH3** DOMAIN; VESICLES; IDENTIFICATION; **ENDOCYTOSIS**; INTERACTS; GENE

Research Fronts: 95-1528 001 (BASIC HELIX-LOOP-HELIX PROTEIN; MYOD FAMILY OF GENE REGULATORY FACTORS; **MOUSE** MRF4 PROMOTER; MYOGENIN EXPRESSION; MAX INTERACTION SPECIFICITY)
95-4415 001 (ELECTROSTATIC REPULSIONS IN THE 2...

9/3,K,AB/3 (Item 2 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci

05443713 Genuine Article#: VZ316 Number of References: 86
Title: A NOVEL FLUORESCENCE-ACTIVATED CELL SORTER-BASED SCREEN FOR YEAST **ENDOCYTOSIS** MUTANTS IDENTIFIES A YEAST HOMOLOG OF **MAMMALIAN** EPS15 (Abstract Available)
Author(s): WENDLAND B; MCCAFFERY JM; XIAO Q; EMR SD
Corporate Source: UNIV CALIF SAN DIEGO,SCH MED,HOWARD HUGHES MED INST,DIV CELL & MOL MED/LA JOLLA//CA/92093; UNIV CALIF SAN DIEGO,SCH MED,HOWARD HUGHES MED INST,DIV CELL & MOL MED/LA JOLLA//CA/92093
Journal: JOURNAL OF CELL BIOLOGY, **1996**, V135, N6 (DEC), P1485-1500
ISSN: 0021-9525
Language: ENGLISH Document Type: ARTICLE
Abstract: A complete understanding of the molecular mechanisms of **endocytosis** requires the discovery and characterization of the protein machinery that mediates this aspect of membrane trafficking. A novel genetic screen was used to identify yeast mutants defective in internalization of bulk lipid. The fluorescent lipophilic styryl dye FM4-64 was used in conjunction with FACS(R) to enrich for yeast mutants that exhibit internalization defects. Detailed characterization of two of these mutants, dim1-1 and dim2-1, revealed defects in the endocytic pathway. Like other yeast **endocytosis** mutants, the temperature-sensitive dim mutants were unable to endocytose FM4-64 or radiolabeled alpha-factor as efficiently as wild-type cells. In addition, double mutants with either dim1-Delta or dim2-1 and the **endocytosis** mutants end4-1 or act1-1 displayed synthetic growth defects, indicating that the DIM gene products function in a common or parallel endocytic pathway. Complementation cloning of the DIM genes revealed identity of DIM1 to SHE4 and DIM2 to PAN1. Pan1p shares homology with the **mammalian** clathrin adaptor-associated protein, eps15. Both proteins contain multiple **EH** (eps15 homology) domains, a motif proposed to mediate protein-protein interactions. Phalloidin labeling of filamentous actin revealed profound defects in the actin cytoskeleton in both dim mutants. EM analysis revealed that the dim mutants accumulate vesicles and tubulo-vesicular structures reminiscent of **mammalian** early endosomes. In addition, the accumulation of novel plasma membrane invaginations where **endocytosis** is likely to occur were visualized in the mutants by electron microscopy using cationized ferritin as a marker for the endocytic pathway. This new screening strategy demonstrates a role for She4p and Pan1p in **endocytosis**, and provides a new general method for the identification of additional **endocytosis** mutants.

Title: A NOVEL FLUORESCENCE-ACTIVATED CELL SORTER-BASED SCREEN FOR YEAST **ENDOCYTOSIS** MUTANTS IDENTIFIES A YEAST HOMOLOG OF **MAMMALIAN** EPS15
, **1996**
Abstract: A complete understanding of the molecular mechanisms of **endocytosis** requires the discovery and characterization of the protein machinery that mediates this aspect of membrane...

...mutants, dim1-1 and dim2-1, revealed defects in the endocytic pathway. Like other yeast **endocytosis** mutants, the temperature-sensitive dim mutants were unable to endocytose FM4-64 or radiolabeled alpha...

...type cells. In addition, double mutants with either dim1-Delta or dim2-1

and the **endocytosis** mutants end4-1 or act1-1 displayed synthetic growth defects, indicating that the DIM gene...

...revealed identity of DIM1 to SHE4 and DIM2 to PAN1. Pan1p shares homology with the **mammalian** clathrin adaptor-associated protein, eps15. Both proteins contain multiple **EH** (eps15 homology) domains, a motif proposed to mediate protein-protein interactions. Phalloidin labeling of filamentous...

...EM analysis revealed that the dim mutants accumulate vesicles and tubulo-vesicular structures reminiscent of **mammalian** early endosomes. In addition, the accumulation of novel plasma membrane invaginations where **endocytosis** is likely to occur were visualized in the mutants by electron microscopy using cationized ferritin...

...the endocytic pathway. This new screening strategy demonstrates a role for She4p and Pan1p in **endocytosis**, and provides a new general method for the identification of additional **endocytosis** mutants.
...Identifiers--VACUOLAR H+-ATPASE; RECEPTOR-MEDIATED **ENDOCYTOSIS**; TEMPERATURE-SENSITIVE MUTANT; TYROSINE KINASE SUBSTRATE; EPIDERMAL GROWTH-FACTOR; SACCHAROMYCES-CEREVISIAE; ACTIN CYTOSKELETON; INTERNALIZATION STEP...
Research Fronts: 95-4290 002 (N-TERMINAL **SH3** DOMAIN; PROTEIN PRODUCT OF THE C-CBL PROTOONCOGENE; TYROSINE KINASES; BINDING IN-VITRO; PROLINE-RICH...
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S3         76   S1 AND S2
S4      44776   ENDOCYTOSIS
S5         46   S3 AND S4
S6   15061011   MAMMALIAN OR MOUSE OR HUMAN OR RAT
S7         30   S5 AND S6
S8          4   S7 AND PY<=1998
S9          3   RD (unique items)
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     S10     550  EPS15 OR EPS15R
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Processing
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          370554  MURINE
          988300  MOUSE
        12569368  HUMAN
         2116815  RAT
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>>>Records from unsupported files will be retained in the RD set.
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 15/3,K,AB/1     (Item 1 from file: 155)
DIALOG(R)File 155:MEDLINE(R)
(c) format only 2003 The Dialog Corp. All rts. reserv.

11597797   99030416   PMID: 9813051
   Intersectin,  a  novel adaptor protein with two Eps15 homology and
five Src homology 3 domains.
  Yamabhai  M;  Hoffman  N  G;  Hardison  N L; McPherson P S; Castagnoli L;
Cesareni G; Kay B K
  Department  of  Pharmacology, University of Wisconsin, Madison, Wisconsin
53706-1532, USA.
  Journal of biological chemistry (UNITED STATES)   Nov 20 1998,  273
  (47)  p31401-7,  ISSN 0021-9258   Journal Code: 2985121R
  Document type: Journal Article
  Languages: ENGLISH
  Main Citation Owner: NLM
  Record type: Completed
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We screened a Xenopus laevis oocyte cDNA expression library with a Src homology 3 (**SH3**) class II peptide ligand and identified a 1270-amino acid-long protein containing two **Eps15** homology (**EH**) domains, a central coiled-coil region, and five **SH3** domains. We named this protein Intersectin, because it potentially brings together **EH** and **SH3** domain-binding proteins into a macromolecular complex. The ligand preference of the **EH** domains were deduced to be asparajine-proline-phenylalanine (NPF) or cyclized NPF (CX1-2NPFXXC), depending on the type of phage-displayed combinatorial peptide library used. Screens of a **mouse** embryo cDNA library with the **EH** domains of Intersectin yielded clones for the Rev-associated binding/Rev-interacting protein (RAB/Rip) and two novel proteins, which we named Intersectin-binding proteins (Ibps) 1 and 2. All three proteins contain internal and C-terminal NPF peptide sequences, and Ibp1 and Ibp2 also contain putative clathrin-binding sites. Deletion of the C-terminal sequence, NPFL-COOH, from RAB/Rip eliminated **EH** domain binding, whereas fusion of the same peptide sequence to glutathione S-transferase generated strong binding to the **EH** domains of Intersectin. Several experiments support the conclusion that the free carboxylate group contributes to binding of the NPFL motif at the C terminus of RAB/Rip to the **EH** domains of Intersectin. Finally, affinity selection experiments with the **SH3** domains of Intersectin identified two endocytic proteins, dynamin and synaptojanin, as potential interacting proteins. We propose that Intersectin is a component of the endocytic machinery.

Intersectin, a novel adaptor protein with two **Eps15** homology and five Src homology 3 domains.
Nov 20 **1998**,
We screened a Xenopus laevis oocyte cDNA expression library with a Src homology 3 (**SH3**) class II peptide ligand and identified a 1270-amino acid-long protein containing two **Eps15** homology (**EH**) domains, a central coiled-coil region, and five **SH3** domains. We named this protein Intersectin, because it potentially brings together **EH** and **SH3** domain-binding proteins into a macromolecular complex. The ligand preference of the **EH** domains were deduced to be asparajine-proline-phenylalanine (NPF) or cyclized NPF (CX1-2NPFXXC), depending on the type of phage-displayed combinatorial peptide library used. Screens of a **mouse** embryo cDNA library with the **EH** domains of Intersectin yielded clones for the Rev-associated binding/Rev-interacting protein (RAB/Rip...

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...Tags: **Human**;
...; GE; DNA-Binding Proteins--metabolism--ME; Dynamins; Endocytosis; GTP Phosphohydrolases--metabolism--ME; Gene Library; Ligands; **Mice**; Molecular Sequence Data; Nerve Tissue Proteins--metabolism--ME; Oligopeptides; Oocytes; Peptide Library; Phosphoric Monoester Hydrolases...
...Chemical Name: Proteins; Carrier Proteins; DNA-Binding Proteins; Ligands; Nerve Tissue Proteins; Oligopeptides; Peptide Library; Phosphoproteins; Proteins; **eps15** protein; initiator-binding protein 1 ; initiator-binding protein 2; intersectin; receptor interacting protein; uncoating protein...

15/3,K,AB/2 (Item 2 from file: 155)

DIALOG(R)File 155:MEDLINE(R)

11585768 99017974 PMID: 9799604

Two isoforms of a **human** intersectin (ITSN) protein are produced by brain-specific alternative splicing in a stop codon.

Guipponi M; Scott H S; Chen H; Schebesta A; Rossier C; Antonarakis S E
Department of Genetics and Microbiology, University of Geneva Medical School, Geneva 4, 1211.

Genomics (UNITED STATES) Nov 1 **1998**, 53 (3) p369-76, ISSN 0888-7543 Journal Code: 8800135
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed

Using selected trapped exons with homology to specific protein domains, we identified a new full-length cDNA encoding a protein containing many motifs for protein-protein interactions. There are two major mRNA transcripts, a ubiquitously expressed mRNA of 5.3 kb and a brain-specific transcript of approximately 15 kb, encoding proteins of 1220 and 1721 amino acids, respectively. The stop codon of the ORF of the shorter transcript is split between adjacent exons. In brain tissues the last exon of the short transcript is skipped, and an alternative downstream exon, the first of several additional, is used to produce the 15-kb mRNA. The putative **human** protein is highly homologous to Xenopus intersectin (81% identical) and to Drosophila dynamin-associated protein, Dap160 (31% identical) and was termed intersectin (ITSN). Both **human** proteins contain five **SH3** (Src homology 3) domains, two **EH** (**Eps15** homology) domains, and an alpha-helix-forming region. The brain-specific long transcript encodes for three additional domains: a GEF (guanine-nucleotide exchange factors), a PH (pleckstrin homology), and a C2 domain. The Drosophila homologue is associated with dynamin, a protein family involved in the endocytic pathway and/or synaptic vesicle recycling. The structure of the **human** ITSN protein is consistent with its involvement in membrane-associated molecular trafficking and signal transduction pathways. The **human** ITSN gene has been mapped to 21q22.1-q22.2 between markers D21S319 and D21S65, and its importance in Down syndrome and monogenic disorders is currently unknown. Copyright 1998 Academic Press.

Two isoforms of a **human** intersectin (ITSN) protein are produced by brain-specific alternative splicing in a stop codon.

Nov 1 **1998**,

... the first of several additional, is used to produce the 15-kb mRNA. The putative **human** protein is highly homologous to Xenopus intersectin (81% identical) and to Drosophila dynamin-associated protein, Dap160 (31% identical) and was termed intersectin (ITSN). Both **human** proteins contain five **SH3** (Src homology 3) domains, two **EH** (**Eps15** homology) domains, and an alpha-helix-forming region. The brain-specific long transcript encodes for...

... family involved in the endocytic pathway and/or synaptic vesicle recycling. The structure of the **human** ITSN protein is consistent with its involvement in membrane-associated molecular trafficking and signal transduction pathways. The **human** ITSN gene has been mapped to 21q22.1-q22.2 between markers D21S319 and D21S65...

...Tags: **Human**;

; Amino Acid Sequence; Base Sequence; Chromosome Mapping; Chromosomes, **Human**, Pair 21--genetics--GE; Cloning, Molecular; Codon, Terminator --genetics--GE; DNA Primers--genetics--GE; DNA...

15/3,K,AB/3 (Item 3 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

11182484 98058900 PMID: 9395447
An Eps homology (**EH**) domain protein that binds to the Ral-GTPase target, RalBP1.
Yamaguchi A; Urano T; Goi T; Feig L A
Department of Biochemistry, Tufts University School of Medicine, Boston, Massachusetts 02111, USA.
Journal of biological chemistry (UNITED STATES) Dec 12 **1997**, 272 (50) p31230-4, ISSN 0021-9258 Journal Code: 2985121R
Contract/Grant No.: GM47707; GM; NIGMS
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
Ral proteins constitute a family of small GTPases that can be activated by Ras in cells. In the GTP-bound state, Ral proteins bind to RalBP1, a GTPase-activating protein for CDC42 and Rac GTPases. We have used the two-hybrid system in yeast to clone a cDNA for a novel approximately 85-kDa protein that can bind to an additional site on RalBP1. This newly identified protein contains an Eps homology (**EH**) domain, which was first detected in the epidermal growth factor (EGF) receptor substrate **Eps15**. Recently, the **EH** domain of **Eps15** has been shown to bind to proteins containing an asparagine-proline-phenylalanine motif. Moreover, **EH** domains have been found in proteins involved in endocytosis and/or actin cytoskeleton regulation. The RalBP1 associated Eps-homology domain protein, Reps1, is tyrosine-phosphorylated in response to EGF stimulation of cells. In addition, Reps1 has the capacity to form a complex with the **SH3** domains of the adapter proteins Crk and Grb2, which may link Reps1 to an EGF-responsive tyrosine kinase. Thus, Reps1 may coordinate the cellular actions of activated EGF receptors and Ral-GTPases.

An Eps homology (**EH**) domain protein that binds to the Ral-GTPase target, RalBP1.
Dec 12 **1997**,
... bind to an additional site on RalBP1. This newly identified protein contains an Eps homology (**EH**) domain, which was first detected in the epidermal growth factor (EGF) receptor substrate **Eps15**. Recently, the **EH** domain of **Eps15** has been shown to bind to proteins containing an asparagine-proline-phenylalanine motif. Moreover, **EH** domains have been found in proteins involved in endocytosis and/or actin cytoskeleton regulation. The...

... stimulation of cells. In addition, Reps1 has the capacity to form a complex with the **SH3** domains of the adapter proteins Crk and Grb2, which may link Reps1 to an EGF...
...; genetics--GE; Cell Line; Cloning, Molecular; DNA, Complementary --chemistry--CH; Epidermal Growth Factor--metabolism--ME; **Mice**; Molecular Sequence Data; Phosphorylation; Tyrosine--metabolism--ME; src Homology Domains

15/3,K,AB/4 (Item 1 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci

06116898 Genuine Article#: XV956 Number of References: 48
Title: Binding specificity and in vivo targets of the **EH** domain, a novel protein-protein interaction module (ABSTRACT AVAILABLE)
Author(s): Salcini AE; Confalonieri S; Doria M; Santolini E; Tassi E; Minenkova O; Cesareni G; Pelicci PG; DiFiore PP (REPRINT)
Corporate Source: EUROPEAN INST ONCOL,DEPT EXPT ONCOL/I-20140 MILAN//ITALY/ (REPRINT); UNIV ROMA TOR VERGATA,DIPARTIMENTO BIOL/I-00100 ROME//ITALY/ ; EUROPEAN INST ONCOL,DEPT EXPT ONCOL/I-20140 MILAN//ITALY/; UNIV

PARMA,IST PATOL SPECIALE MED/I-43100 PARMA//ITALY/; UNIV BARI,INST MICROBIOL/I-70100 BARI//ITALY/
Journal: GENES & DEVELOPMENT, **1997**, V11, N17 (SEP 1), P2239-2249
ISSN: 0890-9369 Publication date: 19970901
Publisher: COLD SPRING HARBOR LAB PRESS, 1 BUNGTOWN RD, PLAINVIEW, NY 11724
Language: English Document Type: ARTICLE
Abstract: **EH** is a recently identified protein-protein interaction domain found in the signal transducers **Eps15** and **Eps15R** and several other proteins of yeast nematode. We show that **EH** domains from **Eps15** and **Eps15R** bind in vitro to peptides containing an asparagine-proline-phenylalanine (NPF) motif. Direct screening of expression libraries with **EH** domains yielded a number of putative **EH** interactors, all of which possessed NPF motifs that were shown to be responsible for the interaction. Among these interactors were the **human** homolog of NUMB, a developmentally reguated gene of Drosophila, and RAB, the cellular cofactor of the HIV REV protein. We demonstrated coimmunoprecipitation of **Eps15** with NUMB and RAB. Finally, in vitro binding of NPF-containing peptides to cellular proteins and EST database screening established the existence of a family of **EH**-containing proteins in mammals. Eased on the characteristics of **EH**-containing and ED-binding proteins, we propose that **EH** domains are involved in processes connected with the transport and sorting of molecules within the cell.

Title: Binding specificity and in vivo targets of the **EH** domain, a novel protein-protein interaction module
, **1997**
Abstract: **EH** is a recently identified protein-protein interaction domain found in the signal transducers **Eps15** and **Eps15R** and several other proteins of yeast nematode. We show that **EH** domains from **Eps15** and **Eps15R** bind in vitro to peptides containing an asparagine-proline-phenylalanine (NPF) motif. Direct screening of expression libraries with **EH** domains yielded a number of putative **EH** interactors, all of which possessed NPF motifs that were shown to be responsible for the interaction. Among these interactors were the **human** homolog of NUMB, a developmentally reguated gene of Drosophila, and RAB, the cellular cofactor of the HIV REV protein. We demonstrated coimmunoprecipitation of **Eps15** with NUMB and RAB. Finally, in vitro binding of NPF-containing peptides to cellular proteins and EST database screening established the existence of a family of **EH**-containing proteins in mammals. Eased on the characteristics of **EH**-containing and ED-binding proteins, we propose that **EH** domains are involved in processes connected with the transport and sorting of molecules within the...
...Identifiers--TYROSINE KINASE SUBSTRATE; SRC HOMOLOGY-3 DOMAINS; **SH3** DOMAIN; SACCHAROMYCES-CEREVISIAE; ASYMMETRIC LOCALIZATION; SIGNAL-TRANSDUCTION; ACTIN CYTOSKELETON; TERMINAL DOMAIN; **MAMMALIAN** NUMB; GENE ENCODES
Research Fronts: 95-4290 007 (N-TERMINAL **SH3** DOMAIN; PROTEIN PRODUCT OF THE C-CBL PROTOONCOGENE; TYROSINE KINASES; BINDING IN-VITRO; PROLINE-RICH...

15/3,K,AB/5 (Item 2 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci

05443713 Genuine Article#: VZ316 Number of References: 86
Title: A NOVEL FLUORESCENCE-ACTIVATED CELL SORTER-BASED SCREEN FOR YEAST ENDOCYTOSIS MUTANTS IDENTIFIES A YEAST HOMOLOG OF **MAMMALIAN** **EPS15** (Abstract Available)
Author(s): WENDLAND B; MCCAFFERY JM; XIAO Q; EMR SD
Corporate Source: UNIV CALIF SAN DIEGO,SCH MED,HOWARD HUGHES MED INST,DIV CELL & MOL MED/LA JOLLA//CA/92093; UNIV CALIF SAN DIEGO,SCH MED,HOWARD

HUGHES MED INST,DIV CELL & MOL MED/LA JOLLA//CA/92093
Journal: JOURNAL OF CELL BIOLOGY, **1996**, V135, N6 (DEC), P1485-1500
ISSN: 0021-9525
Language: ENGLISH Document Type: ARTICLE
Abstract: A complete understanding of the molecular mechanisms of endocytosis requires the discovery and characterization of the protein machinery that mediates this aspect of membrane trafficking. A novel genetic screen was used to identify yeast mutants defective in internalization of bulk lipid. The fluorescent lipophilic styryl dye FM4-64 was used in conjunction with FACS(R) to enrich for yeast mutants that exhibit internalization defects. Detailed characterization of two of these mutants, dim1-1 and dim2-1, revealed defects in the endocytic pathway. Like other yeast endocytosis mutants, the temperature-sensitive dim mutants were unable to endocytose FM4-64 or radiolabeled alpha-factor as efficiently as wild-type cells. In addition, double mutants with either dim1-Delta or dim2-1 and the endocytosis mutants end4-1 or act1-1 displayed synthetic growth defects, indicating that the DIM gene products function in a common or parallel endocytic pathway. Complementation cloning of the DIM genes revealed identity of DIM1 to SHE4 and DIM2 to PAN1. Pan1p shares homology with the **mammalian** clathrin adaptor-associated protein, **eps15**. Both proteins contain multiple **EH** (**eps15** homology) domains, a motif proposed to mediate protein-protein interactions. Phalloidin labeling of filamentous actin revealed profound defects in the actin cytoskeleton in both dim mutants. EM analysis revealed that the dim mutants accumulate vesicles and tubulo-vesicular structures reminiscent of **mammalian** early endosomes. In addition, the accumulation of novel plasma membrane invaginations where endocytosis is likely to occur were visualized in the mutants by electron microscopy using cationized ferritin as a marker for the endocytic pathway. This new screening strategy demonstrates a role for She4p and Pan1p in endocytosis, and provides a new general method for the identification of additional endocytosis mutants.

...Title: FLUORESCENCE-ACTIVATED CELL SORTER-BASED SCREEN FOR YEAST ENDOCYTOSIS MUTANTS IDENTIFIES A YEAST HOMOLOG OF **MAMMALIAN EPS15**
, 1996
...Abstract: revealed identity of DIM1 to SHE4 and DIM2 to PAN1. Pan1p shares homology with the **mammalian** clathrin adaptor-associated protein, **eps15**. Both proteins contain multiple **EH** (**eps15** homology) domains, a motif proposed to mediate protein-protein interactions. Phalloidin labeling of filamentous actin ...

...EM analysis revealed that the dim mutants accumulate vesicles and tubulo-vesicular structures reminiscent of **mammalian** early endosomes. In addition, the accumulation of novel plasma membrane invaginations where endocytosis is likely...
Research Fronts: 95-4290 002 (N-TERMINAL **SH3** DOMAIN; PROTEIN PRODUCT OF THE C-CBL PROTOONCOGENE; TYROSINE KINASES; BINDING IN-VITRO; PROLINE-RICH...
?

13/3,K,AB/13 (Item 13 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

07873073 93328758 PMID: 8101525

Mutations in **human dynamin** block an intermediate stage in coated vesicle formation.

van der Bliek A M; Redelmeier T E; Damke H; Tisdale E J; Meyerowitz E M; Schmid S L

Division of Biology, California Institute of Technology, Pasadena 91125.

Journal of cell biology (UNITED STATES) Aug **1993**, 122 (3) p553-63, ISSN 0021-9525 Journal Code: 0375356

Contract/Grant No.: CA09270; CA; NCI; GM40499; GM; NIGMS; GM42445; GM; NIGMS

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

The role of **human dynamin** in receptor-mediated endocytosis was investigated by transient expression of GTP-binding domain mutants in mammalian cells. Using assays which detect intermediates in coated vesicle formation, the dynamin mutants were found to block endocytosis at a stage after the initiation of coat assembly and preceding the sequestration of ligands into deeply invaginated coated pits. Membrane transport from the ER to the Golgi complex was unaffected indicating that dynamin mutants specifically block early events in endocytosis. These results demonstrate that mutations in the GTP-binding domain of dynamin block Tfn-endocytosis in mammalian cells and suggest that a functional dynamin GTPase is required for receptor-mediated endocytosis via clathrin-coated pits.

Mutations in **human dynamin** block an intermediate stage in

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S4        370   S3 AND PY<=1998
S5      50156   EH
S6         43   S3 AND S5
S7      10728   SH3
S8         28   S6 AND S7
S9         12   RD (unique items)
S10         2   S9 AND PY<=1998
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            3330  DYNAMIN
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SYSTEM:OS  - DIALOG OneSearch
  File 155:MEDLINE(R)  1966-2004/Jan W1
         (c) format only 2003 The Dialog Corp.
*File 155: Medline is updating again (12-22-2003).
Please see HELP NEWS 154, for details.
  File  55:Biosis Previews(R)  1993-2003/Dec W4
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  File  34:SciSearch(R) Cited Ref Sci  1990-2003/Dec W4
         (c) 2003 Inst for Sci Info
*File  34: New prices as of 1/1/2004 per Information Provider
request.  See HELP RATES 34.
  File 434:SciSearch(R) Cited Ref Sci  1974-1989/Dec
         (c) 1998 Inst for Sci Info
*File 434: New prices as of 1/1/2004 per Information Provider
request.  See HELP RATES434.
  File 340:CLAIMS(R)/US Patent  1950-03/Dec 30
         (c) 2004 IFI/CLAIMS(R)
*File 340: Enter HELP NEWS340 & HELP ALERTS340 for search,
 display & Alert information.

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            7235  EPS
         2920049  15
              23  EPS(W)15
      S1     562  EPS15 OR EPS(W)15
? s human
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             562  S1
        12569368  S2
      S3     170  S1 AND S2
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Processing
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>>>Records from unsupported files will be retained in the RD set.
...completed examining records
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? t s5/3,k,ab/20-23

 5/3,K,AB/20     (Item 6 from file: 55)
DIALOG(R)File  55:Biosis Previews(R)
(c) 2003 BIOSIS. All rts. reserv.

0009902455   BIOSIS NO.: 199598370288
The SH3 Domain of Crk Binds Specifically to a Conserved Proline-rich Motif
  in Eps15 and Eps15R
AUTHOR: Schumacher Christoph; Knudsen Beatrice S; Ohuchi Tohru; Di Fiore
  Pier Paolo; Glassman Robert H; Hanafusa Hidesaburo (Reprint)
AUTHOR ADDRESS: Lab. Mol. Oncol., Rockefeller University, 1230 York Ave.,
  New York, NY 10021, USA**USA
JOURNAL: Journal of Biological Chemistry  270 (25): p15341-15347 1995
1995
ISSN: 0021-9258
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
```

LANGUAGE: English

ABSTRACT: The Crk protein belongs to the family of proteins consisting of mainly Src homology 2 and 3 (SH2 and SH3) domains. These proteins are thought to transduce signals from tyrosine kinases to downstream effectors. In order to understand the specificity and effector function of the SH3 domain of Crk, we screened an expression library for binding proteins. We isolated **Eps15**, a substrate of the epidermal growth factor receptor (EGFR) tyrosine kinase, and Eps15R, a novel protein with high sequence homology to the carboxyl-terminal domain of **Eps15**. Antibodies raised against a fragment of the Eps15R gene product immunoprecipitated a protein of 145 kDa. **Eps15** and Eps15R bound specifically to the amino-terminal SH3 domain of Crk and coprecipitated equivalently with both c-Crk and v-Crk from cell lysates. The amino acid sequences of **Eps15** and Eps15R featured several proline-rich regions as putative binding motifs for SH3 domains. In both **Eps15** and Eps15R, we identified one proline-rich motif which accounts for their interaction with the Crk SH3 domain. Each binding motif contains the sequence P-X-L-P-X-K, an amino acid stretch that is highly conserved in all proteins known to interact specifically with the first SH3 domain of Crk. Furthermore, we found that immunoprecipitates of activated EGFR-kinase stably bound in vitro-translated **Eps15** only in the presence of in vitro-translated v-Crk. Crk might therefore be involved in **Eps15**-mediated signal transduction through the EGFR.

The SH3 Domain of Crk Binds Specifically to a Conserved Proline-rich Motif in **Eps15** and Eps15R
1995

...ABSTRACT: the SH3 domain of Crk, we screened an expression library for binding proteins. We isolated **Eps15**, a substrate of the epidermal growth factor receptor (EGFR) tyrosine kinase, and Eps15R, a novel protein with high sequence homology to the carboxyl-terminal domain of **Eps15**. Antibodies raised against a fragment of the Eps15R gene product immunoprecipitated a protein of 145 kDa. **Eps15** and Eps15R bound specifically to the amino-terminal SH3 domain of Crk and coprecipitated equivalently with both c-Crk and v-Crk from cell lysates. The amino acid sequences of **Eps15** and Eps15R featured several proline-rich regions as putative binding motifs for SH3 domains. In both **Eps15** and Eps15R, we identified one proline-rich motif which accounts for their interaction with the...

...Crk. Furthermore, we found that immunoprecipitates of activated EGFR-kinase stably bound in vitro-translated **Eps15** only in the presence of in vitro-translated v-Crk. Crk might therefore be involved in **Eps15**-mediated signal transduction through the EGFR.
DESCRIPTORS:
ORGANISMS: **human** (Hominidae...

5/3,K,AB/21 (Item 7 from file: 55)
DIALOG(R)File 55:Biosis Previews(R)

0009522334 BIOSIS NO.: 199497543619
Multiple cytokines stimulate the binding of a common 145-kilodalton protein to Shc at the Grb2 recognition site on Shc
AUTHOR: Liu Ling; Damen Jacqueline E; Cutler Robert L; Krystal Gerald (Reprint)
AUTHOR ADDRESS: Terry Fox Lab., BC Cancer Res. Centre, 601 West 10th Ave., Vancouver, BC V5Z 1L3, Canada**Canada
JOURNAL: Molecular and Cellular Biology 14 (10): p6926-6935 1994
1994

ISSN: 0270-7306
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: We recently reported that interleukin-3, Steel factor, and erythropoietin all induce the tyrosine phosphorylation of Shc and its association with Grb2 in hemopoietic cell lines. We have now further characterized the proteins that become associated with Shc following stimulation with these cytokines and found that, in response to all three, the tyrosine-phosphorylated form of Shc binds to common 145- and 52-kDa proteins which also become tyrosine phosphorylated in response to these growth factors. The 145-kDa protein, which appears, from antiphosphotyrosine blots of two-dimensional O'Farrell gels, to exist in four different phosphorylation states following cytokine stimulation (with isoelectric points ranging from 7.2 to 7.8), does not appear to be immunologically related to the beta subunit of the interleukin-3 receptor, c-Kit, BCR, ABL, JAK1, JAK2, Sos1, **eps15**, or insulin receptor substrate 1 protein. Silver-stained sodium dodecyl sulfate gels indicate that the association of the 145-kDa protein with Shc occurs only after cytokine stimulation and that it can bind to the tyrosine-phosphorylated form of Shc in its non-tyrosine-phosphorylated state. The latter finding, in conjunction with the observations that p145 does not bind, in vitro, to the Src homology 2 (SH2) domain of Shc, that it is not present in anti-Grb2 immunoprecipitates, and that a phosphopeptide which blocks the binding of Shc to the SH2 domain of Grb2 also blocks the binding of Shc to p145, suggests that p145 contains an SH2 domain and competes with Grb2 for the same tyrosine-phosphorylated site on She. This implicates p145 as a potential regulator of Ras activity and, perhaps, of other as yet unidentified functions of Shc.

1994
...ABSTRACT: the beta subunit of the interleukin-3 receptor, c-Kit, BCR, ABL, JAK1, JAK2, Sos1, **eps15**, or insulin receptor substrate 1 protein. Silver-stained sodium dodecyl sulfate gels indicate that the...
DESCRIPTORS:
ORGANISMS: **human** (Hominidae...

5/3,K,AB/22 (Item 1 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci

03193223 Genuine Article#: NL815 Number of References: 49
Title: THE **HUMAN EPS15** GENE, ENCODING A TYROSINE KINASE SUBSTRATE, IS CONSERVED IN EVOLUTION AND MAPS TO 1P31-P-32 (Abstract Available)
Author(s): WONG WT; KRAUS MH; CARLOMAGNO F; ZELANO A; DRUCK T; CROCE CM; HUEBNER K; DIFIORE PP
Corporate Source: NCI,CELLULAR & MOLEC BIOL LAB,BLDG 37/BETHESDA//MD/20892; NCI,CELLULAR & MOLEC BIOL LAB/BETHESDA//MD/20892; THOMAS JEFFERSON UNIV,JEFFERSON MED COLL,JEFFERSON INST MOLEC MED/PHILADELPHIA//PA/19107
Journal: ONCOGENE, **1994**, V9, N6 (JUN), P1591-1597
ISSN: 0950-9232
Language: ENGLISH Document Type: ARTICLE
Abstract: Employing an expression cloning approach for tyrosine kinase substrates, we have previously isolated the coding sequence for a novel putative EGFR substrate, **eps15**, from NIH3T3 fibroblasts. **Eps15** displayed a receptor-specific pattern of tyrosine phosphorylation in vivo and was able to transform NIH3T3 cells upon overexpression. To gain understanding of **eps15** function as well as its role in normal and neoplastic proliferation, we cloned the **human eps15** coding sequence and studied expression of the

human RNA and protein, evolutionary conservation, and chromosomal location. The close structural similarity of **human eps15** with the murine homologue is indicated by 89% and 90% identity of nucleotide and predicted amino acid sequences, respectively. Using the **human eps15** coding sequence as probe, we demonstrate that **eps15** is member of a gene family that is highly conserved during evolution. An essential function of **eps15** in cell growth regulation is underscored by our observation of ubiquitous expression at the transcript and the protein level in normal and malignant **human** cells. The **human EPS15** locus maps to chromosome 1p31-p32, a region involved in deletion in neuroblastoma, translocations in acute lymphoblastic leukemia, and exhibiting a fragile site.

Title: THE **HUMAN EPS15** GENE, ENCODING A TYROSINE KINASE SUBSTRATE, IS CONSERVED IN EVOLUTION AND MAPS TO 1P31-P...
, 1994
...Abstract: kinase substrates, we have previously isolated the coding sequence for a novel putative EGFR substrate, **eps15**, from NIH3T3 fibroblasts. **Eps15** displayed a receptor-specific pattern of tyrosine phosphorylation in vivo and was able to transform NIH3T3 cells upon overexpression. To gain understanding of **eps15** function as well as its role in normal and neoplastic proliferation, we cloned the **human eps15** coding sequence and studied expression of the **human** RNA and protein, evolutionary conservation, and chromosomal location. The close structural similarity of **human eps15** with the murine homologue is indicated by 89% and 90% identity of nucleotide and predicted amino acid sequences, respectively. Using the **human eps15** coding sequence as probe, we demonstrate that **eps15** is member of a gene family that is highly conserved during evolution. An essential function of **eps15** in cell growth regulation is underscored by our observation of ubiquitous expression at the transcript and the protein level in normal and malignant **human** cells. The **human EPS15** locus maps to chromosome 1p31-p32, a region involved in deletion in neuroblastoma, translocations in...

5/3,K,AB/23 (Item 1 from file: 340)
DIALOG(R)File 340:CLAIMS(R)/US Patent

Dialog Acc No: 2686136 IFI Acc No: 9602431
Document Type: C
DNA ENCODING **HUMAN** AND MURINE **EPS15**, A SUBSTRATE FOR THE EPIDERMAL GROWTH FACTOR RECEPTOR; GENETIC ENGINEERING AND CELLS
Inventors: DiFiore Pier P (US); Fazioli Francesca (IT)
Assignee: U S of America Health & Human Services
Assignee Code: 06814
Publication (No,Date), Applic (No,Date):
US 5487979 **19960130** US 9395737 19930722
Publication Kind: A
Calculated Expiration: 20130130
(Cited in 001 later patents)
Cont.-in-part Pub(No),Applic(No,Date): US 5378809 US 92935311 19920825
Priority Applic(No,Date): US 9395737 19930722; US 92935311 19920825

Abstract: A new substrate of epidermal growth factor receptor and certain other tyrosine kinase receptors denominated **eps15** is disclosed, as well as, polynucleotides encoding **eps15**, antisense **eps15** polynucleotide, triple helix **eps15** polynucleotide, antibodies to **eps15**, and assays for determining **eps15**.

DNA ENCODING **HUMAN** AND MURINE **EPS15**, A SUBSTRATE FOR THE EPIDERMAL GROWTH FACTOR RECEPTOR...
Publication (No,Date), Applic (No,Date):
...**19960130**

Abstract: A new substrate of epidermal growth factor receptor and certain other tyrosine kinase receptors denominated **eps15** is disclosed, as well as, polynucleotides encoding **eps15**, antisense **eps15** polynucleotide, triple helix **eps15** polynucleotide, antibodies to **eps15**, and assays for determining **eps15**.

Exemplary Claim: 1. Isolated or purified polynucleotide operably encoding **human eps15**, wherein said polynucleotide comprises a sequence encoding the amino acid sequence of SEQ ID NO...
Non-exemplary Claims: 2. Isolated or purified polynucleotide operably encoding murine **eps15**, wherein said polynucleotide comprises a sequence encoding the amino acid sequence of SEQ ID NO...

...5. Isolated or purified polynucleotide operably encoding **human eps15**, wherein said polynucleotide is mRNA and comprises a mRNA transcript of the DNA sequence encoding...

...6. Isolated or purified polynucleotide operably encoding murine **eps15**, wherein said polynucleotide is mRNA and comprises a mRNA transcript of the DNA sequence encoding...
?

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? ds

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           50156  S6
      S7     212  S1 AND S6
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? s s7 and s8
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           10728  S8
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? rd
>>>Duplicate detection is not supported for File 340.

>>>Records from unsupported files will be retained in the RD set.
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? t s11/3,k,ab/1-3

 11/3,K,AB/1     (Item 1 from file: 155)
DIALOG(R)File 155:MEDLINE(R)
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11182484   98058900   PMID: 9395447
   An Eps homology (EH) domain protein that binds to the Ral-GTPase
target, RalBP1.
  Yamaguchi A; Urano T; Goi T; Feig L A
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Massachusetts 02111, USA.
  Journal of biological chemistry (UNITED STATES)   Dec 12 1997,  272
  (50)  p31230-4,  ISSN 0021-9258   Journal Code: 2985121R
  Contract/Grant No.: GM47707; GM; NIGMS
  Document type: Journal Article
  Languages: ENGLISH
  Main Citation Owner: NLM
  Record type: Completed
  Ral proteins constitute a family of small GTPases that can be activated
by Ras in cells. In the GTP-bound state, Ral proteins bind to RalBP1, a
GTPase-activating protein for CDC42 and Rac GTPases. We have used the
two-hybrid system in yeast to clone a cDNA for a novel approximately 85-kDa
protein that can bind to an additional site on RalBP1. This newly
identified protein contains an Eps homology (EH) domain, which was
first detected in the epidermal growth factor (EGF) receptor substrate
Eps15. Recently, the EH domain of Eps15 has been shown to
bind to proteins containing an asparagine-proline-phenylalanine motif.
Moreover, EH domains have been found in proteins involved in
endocytosis and/or actin cytoskeleton regulation. The RalBP1 associated
Eps-homology domain protein, Reps1, is tyrosine-phosphorylated in response
to EGF stimulation of cells. In addition, Reps1 has the capacity to form a
complex with the SH3 domains of the adapter proteins Crk and Grb2,
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which may link Reps1 to an EGF-responsive tyrosine kinase. Thus, Reps1 may coordinate the cellular actions of activated EGF receptors and Ral-GTPases.

An Eps homology (**EH**) domain protein that binds to the Ral-GTPase target, RalBP1.
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... stimulation of cells. In addition, Reps1 has the capacity to form a complex with the **SH3** domains of the adapter proteins Crk and Grb2, which may link Reps1 to an EGF...

11/3,K,AB/2 (Item 1 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci

06116898 Genuine Article#: XV956 Number of References: 48
Title: Binding specificity and in vivo targets of the **EH** domain, a novel protein-protein interaction module (ABSTRACT AVAILABLE)
Author(s): Salcini AE; Confalonieri S; Doria M; Santolini E; Tassi E; Minenkova O; Cesareni G; Pelicci PG; DiFiore PP (REPRINT)
Corporate Source: EUROPEAN INST ONCOL,DEPT EXPT ONCOL/I-20140 MILAN//ITALY/ (REPRINT); UNIV ROMA TOR VERGATA,DIPARTIMENTO BIOL/I-00100 ROME//ITALY/ ; EUROPEAN INST ONCOL,DEPT EXPT ONCOL/I-20140 MILAN//ITALY/; UNIV PARMA,IST PATOL SPECIALE MED/I-43100 PARMA//ITALY/; UNIV BARI,INST MICROBIOL/I-70100 BARI//ITALY/
Journal: GENES & DEVELOPMENT, **1997**, V11, N17 (SEP 1), P2239-2249
ISSN: 0890-9369 Publication date: 19970901
Publisher: COLD SPRING HARBOR LAB PRESS, 1 BUNGTOWN RD, PLAINVIEW, NY 11724
Language: English Document Type: ARTICLE
Abstract: **EH** is a recently identified protein-protein interaction domain found in the signal transducers **Eps15** and Eps15R and several other proteins of yeast nematode. We show that **EH** domains from **Eps15** and Eps15R bind in vitro to peptides containing an asparagine-proline-phenylalanine (NPF) motif. Direct screening of expression libraries with **EH** domains yielded a number of putative **EH** interactors, all of which possessed NPF motifs that were shown to be responsible for the interaction. Among these interactors were the human homolog of NUMB, a developmentally reguated gene of Drosophila, and RAB, the cellular cofactor of the HIV REV protein. We demonstrated coimmunoprecipitation of **Eps15** with NUMB and RAB. Finally, in vitro binding of NPF-containing peptides to cellular proteins and EST database screening established the existence of a family of **EH** -containing proteins in mammals. Eased on the characteristics of **EH**-containing and ED-binding proteins, we propose that **EH** domains are involved in processes connected with the transport and sorting of molecules within the cell.

Title: Binding specificity and in vivo targets of the **EH** domain, a novel protein-protein interaction module
, **1997**
Abstract: **EH** is a recently identified protein-protein interaction domain found in the signal transducers **Eps15** and Eps15R and several other proteins of yeast nematode. We show that **EH** domains from **Eps15** and Eps15R bind in vitro to peptides containing an